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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Clinton, Gail M., Doherty, Joni Kristin, and  
5 Adelman, John P.

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 10

10 (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: DAVIS WRIGHT TREMAINE
- (B) STREET: 1501 Fourth Avenue, 2600 Century Square
- (C) CITY: Seattle
- 15 (D) STATE: Washington
- (E) COUNTRY: U.S.A.
- (F) ZIP: 98101

20 (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: PC compatible
- (C) OPERATING SYSTEM: Windows95
- (D) SOFTWARE: Word

25 (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: to be assigned
- (B) FILING DATE: 16 February 2000
- (C) CLASSIFICATION:

30 (viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Oster, Jeffrey B.
- (B) REGISTRATION NUMBER: 32,585
- (C) REFERENCE/DOCKET NUMBER: 49321-1

35 (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206 628 7711
- (B) TELEFAX: 206 628 7699

40 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- 45 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro Xaa  
5 5 10 15  
Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu Arg Pro  
20 25 30  
Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu Ala Pro Leu  
35 40 45  
10 Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val Gly Arg Gly Xaa  
50 55 60  
Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser Arg Tyr Glu Gly  
65 70 75

15 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 419  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

25 Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu Leu  
5 10 15  
Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp Cys Lys  
20 25 30  
Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His  
30 35 40 45  
Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr  
50 55 60  
Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val  
65 70 75  
35 Gln Gly Tyr Val Leu Cys Ala His Asn Gln Val Arg Gln Val Pro Leu  
80 85 90 95  
Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr  
100 105 110  
Ala Leu Ala Val Leu Asp Asn Gly Asp Pro Leu Arg Asn Thr Thr Pro  
40 115 120 125  
Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser  
130 135 140  
Leu Thr Glu Cys Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln  
145 150 155  
45 Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn

	160	165	170	175
	Asn Gln Leu Ala Leu Thr Leu Ile	Asp	Thr Asn Arg Ser Arg Ala Cys	
	180		185	190
5	His Pro Cys Ser Pro Cys Cys Lys	Gly	Ser Arg Cys Trp Gly Glu Ser	
	195		200	205
	Ser Glu Asp Cys Gln Ser Leu	Thr	Arg Thr Val Cys Ala Gly Gly Cys	
	210	215		220
	Ala Arg Cys Lys Gly Pro Leu	Pro	Thr Asp Cys Cys His Glu Gln Cys	
	225	230		235
10	Ala Ala Gly Cys Thr Gly Pro	Lys	His Ser Asp Cys Leu Ala Cys Leu	
	240	245		255
	His Phe Asn His Ser Gly Ile	Cys	Glu Leu His Cys Pro Ala Leu Val	
	260		265	270
	Thr Tyr Asn Thr Asp Thr Phe	Glu	Ser Cys Pro Asn Pro Glu Gly Arg	
15	275		280	285
	Tyr Thr Phe Gly Ala Ser Cys	Val	Thr Ala Cys Pro Tyr Asn Lys Leu	
	290		295	300
	Ser Thr Asp Val Gly Ser Cys	Thr	Leu Val Cys Pro Leu His Asn Gln	
	305	310		315
20	Glu Val Thr Ala Glu Asp Gly	Thr	Gln Arg Cys Glu Lys Cys Ser Lys	
	320	325		335
	Pro Cys Ala Arg Val Gly Xaa	His	Ser Xaa Xaa Pro Arg Pro Ala Ala	
	340		345	350
	Val Pro Val Pro Xaa Arg Xaa	Gln	Pro Xaa Pro Ala His Pro Val Leu	
25	355		360	365
	Ser Phe Leu Arg Pro Ser Trp	Asp	Xaa Val Ser Ala Phe Tyr Ser Leu	
	370		375	380
	Pro Leu Ala Pro Leu Asp	Pro	Thr Ser Val Xaa Ile Ser Pro Val Ser	
	385	390		395
30	Val Gly Arg Gly Xaa Asp	Pro	Asp Ala His Val Ala Val Xaa Leu Ser	
	400	405		410
	Arg Tyr Glu Gly			415

(2) INFORMATION FOR SEQ ID NO:3:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

40 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

45 TGAGCACCAT GGAGCTGGC 19

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(2) INFORMATION FOR SEQ ID NO:4:

5 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

10 TCCGGCAGAA ATGCCAGGCT CC 22

15 (2) INFORMATION FOR SEQ ID NO:5:

15 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

20 AACACAGCGG TGTGAGAAGT GC 22

25 (2) INFORMATION FOR SEQ ID NO:6:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

30 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

30 ATACCGGGAC AGGTCAACAG C 21

35 (2) INFORMATION FOR SEQ ID NO:7:

35 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

40 (ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

45 TCTGGGTACC CACTCACTGC 20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

10 TTCACACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

20 GCACGGATCC ATAGCAGACT GAGGAGG 27

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

25 GGT WCC CAC TCA CYG CYC CCG AGG CCA GCT GCA GTT CCT GTC CCT 45  
Gly Xaa His Ser Xaa Xaa Pro Arg Pro Ala Ala Val Pro Val Pro  
35 5 10 15

40 CWG CGC ATR CAG CCT GNC CCA GCC CAC CCT GTC CTA TCC TTC CTC 90  
Xaa Arg Xaa Gln Pro Xaa Pro Ala His Pro Val Leu Ser Phe Leu  
20 25 30

AGA CCC TCT TGG GAC MTA GTC TCT GCC TTC TAC TCT CTA CCC CTG 135  
Arg Pro Ser Trp Asp Xaa Val Ser Ala Phe Tyr Ser Leu Pro Leu  
35 40 45

45 GCC CCC CTC AGC CCT ACA AGT GTC CST ATA TCC CCT GTC AGT GTG 180

Ala Pro Leu Ser Pro Thr Ser Val Xaa Ile Ser Pro Val Ser Val  
50 55 60

5 GGG AGG GGC CYG GAC CCT GAT GCT CAT GTG GCT GTT SAC CTG TCC 225  
 Gly Arg Gly Xaa Asp Pro Asp Ala His Val Ala Val Xaa Leu Ser  
                   65                  70                  75

CGG TAT GAA GGC TGA 240  
Arg Tyr Glu Gly

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